



SEQUENCE LISTING

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#16

<120> Inhibition of CMV Infection and Dissemination

<130> 019934-002510US

<140> US 09/944,049

<141> 2001-08-30

<150> US 60/229,365

<151> 2000-08-30

<160> 48

<170> PatentIn Ver. 2.1

<210> 1

<211> 1065

<212> DNA

<213> Human cytomegalovirus

<220>

<223> human cytomegalovirus (HCMV) Toledo strain open
reading frame US28 (AU4.1)

<220>

<221> CDS

<222> (1)..(1065)

<223> HCMV Toledo US28

<400> 1

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<210> 2

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<212> PRT

<213> Human cytomegalovirus

<220>

<223> human cytomegalovirus (HCMV) Toledo strain open
reading frame US28 (AU4.1)

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Cys	Leu	Phe	Ser	Ile	Phe	Trp	Trp	Ile	Phe	Ala	Val	Ile	Ile	Ala	Ile
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Pro	His	Phe	Met	Val	Val	Thr	Lys	Lys	Asp	Asn	Gln	Cys	Met	Thr	Asp
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Tyr	Asp	Tyr	Leu	Glu	Val	Ser	Tyr	Pro	Ile	Ile	Leu	Asn	Val	Glu	Leu
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Arg	Ile	Val	Arg	Val	Leu	Ile	Ala	Val	Val	Leu	Val	Phe	Ile	Ile	Phe
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Lys	Trp	Ile	Ser	Ser	Ser	Cys	Glu	Phe	Glu	Arg	Ser	Leu	Lys	Arg	Ala
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Leu	Ile	Leu	Thr	Glu	Ser	Leu	Ala	Phe	Cys	His	Cys	Cys	Leu	Asn	Pro
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Leu Leu Ala Glu Phe Arg Gln Arg Leu Phe Ser Arg Asp Val Ser Trp
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Thr Ser Ser Asp Thr Leu Ser Asp Glu Val Cys Arg Val Ser Gln Ile
 340 345 350

Ile Pro

<210> 3
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 <212> DNA
 <213> Human cytomegalovirus

<220>
 <223> human cytomegalovirus (HCMV) VHL/E strain open
 reading frame US28

<220>
 <221> CDS
 <222> (1)..(1065)
 <223> HCMV VHL/E US28

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 ggcgttgtct ttctcttcgg ttccatcggc aacttcttgg tgatcttcac catcacctgg 180
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 cttttcgttt gtacactacc tctgtggatg caatacctcc tagatcacia ctccctagcc 300
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 tttatcacgg agattgcact cgatcgctac tacgctattg tttacatgag atacggcct 420
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 cgccacaaag gccgcattgt acgggtactt atagcggtcg tgcttgcttt tatcatcttt 720
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<210> 4
 <211> 354
 <212> PRT
 <213> Human cytomegalovirus

<220>
 <223> human cytomegalovirus (HCMV) VHL/E strain open
 reading frame US28

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			20					25					30				
Lys	Pro	Val	Thr	Leu	Phe	Leu	Tyr	Gly	Val	Val	Phe	Leu	Phe	Gly	Ser		
		35					40					45					
Ile	Gly	Asn	Phe	Leu	Val	Ile	Phe	Thr	Ile	Thr	Trp	Arg	Arg	Arg	Ile		
	50					55					60						
Gln	Cys	Ser	Gly	Asp	Val	Tyr	Phe	Ile	Asn	Leu	Ala	Ala	Ala	Asp	Leu		
65					70					75					80		
Leu	Phe	Val	Cys	Thr	Leu	Pro	Leu	Trp	Met	Gln	Tyr	Leu	Leu	Asp	His		
				85					90					95			
Asn	Ser	Leu	Ala	Ser	Val	Pro	Cys	Thr	Leu	Leu	Thr	Ala	Cys	Phe	Tyr		
			100					105						110			
Val	Ala	Met	Phe	Ala	Ser	Leu	Cys	Phe	Ile	Thr	Glu	Ile	Ala	Leu	Asp		
		115					120					125					
Arg	Tyr	Tyr	Ala	Ile	Val	Tyr	Met	Arg	Tyr	Arg	Pro	Val	Lys	Gln	Ala		
	130					135					140						
Cys	Leu	Phe	Ser	Ile	Phe	Trp	Trp	Ile	Phe	Ala	Val	Ile	Ile	Ala	Ile		
145					150					155					160		
Pro	His	Phe	Met	Val	Val	Thr	Lys	Lys	Asp	Asn	Gln	Cys	Met	Thr	Asp		
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Tyr	Asp	Tyr	Leu	Glu	Val	Ser	Tyr	Pro	Ile	Ile	Leu	Asn	Val	Glu	Leu		
			180					185					190				
Met	Leu	Gly	Ala	Phe	Val	Ile	Pro	Leu	Ser	Val	Ile	Ser	Tyr	Cys	Tyr		
		195					200					205					
Tyr	Arg	Ile	Ser	Arg	Ile	Val	Ala	Val	Ser	Gln	Ser	Arg	His	Lys	Gly		
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Arg	Ile	Val	Arg	Val	Leu	Ile	Ala	Val	Val	Leu	Val	Phe	Ile	Ile	Phe		
225					230					235					240		
Trp	Leu	Pro	Tyr	His	Leu	Thr	Leu	Phe	Val	Asp	Thr	Leu	Lys	Leu	Leu		
				245					250					255			
Lys	Trp	Ile	Ser	Ser	Ser	Cys	Glu	Phe	Glu	Lys	Ser	Leu	Lys	Arg	Ala		
			260					265					270				
Leu	Ile	Leu	Thr	Glu	Ser	Leu	Ala	Phe	Cys	His	Cys	Cys	Leu	Asn	Pro		
		275					280					285					
Leu	Leu	Tyr	Val	Phe	Val	Gly	Thr	Lys	Phe	Arg	Gln	Glu	Leu	His	Cys		
		290				295					300						
Leu	Leu	Ala	Glu	Phe	Arg	Gln	Arg	Leu	Phe	Ser	Arg	Asp	Val	Ser	Trp		
305					310					315					320		
Tyr	His	Ser	Met	Ser	Phe	Ser	Arg	Arg	Ser	Ser	Pro	Ser	Arg	Arg	Glu		
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 340 345 350

Ile Pro

<210> 5
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 <213> Rhesus cytomegalovirus

<220>
 <223> rhesus monkey cytomegalovirus (rhCMV) US28 homolog
 rhUS28.1

<220>
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 <222> (1)..(1020)
 <223> rhUS28.1

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 tgcacgtgtg tagtcaagaa acgcaaactg cgatattcca gcgatgttta ttttttccac 180
 gcctctatgg ccgacctcgt cagcactgtc atgctaccgc tctggctaca ttatgtcctc 240
 aactttgccc aactctctcg aggagcctgt atcagctttt cggtgacttt ctatgttccc 300
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 gatttggacc ccgatgccaa tcaattcatg attgaactca ctagccaggg aagaagtaga 960
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<210> 6
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 <212> PRT
 <213> Rhesus cytomegalovirus

<220>
 <223> rhesus monkey cytomegalovirus (rhCMV) US28 homolog
 rhUS28.1

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 35 40 45

Lys Leu Arg Tyr Ser Ser Asp Val Tyr Phe Phe His Ala Ser Met Ala
 50 55 60

Asp Leu Val Ser Thr Val Met Leu Pro Leu Trp Leu His Tyr Val Leu
 65 70 75 80
 Asn Phe Ala Gln Leu Ser Arg Gly Ala Cys Ile Ser Phe Ser Val Thr
 85 90 95
 Phe Tyr Val Pro Leu Phe Val Gln Ala Trp Leu Leu Ile Ser Ile Ala
 100 105 110
 Met Glu Arg Tyr Ser Asn Leu Val Trp Met Ala Pro Ile Ser Val Lys
 115 120 125
 Thr Ala Phe Lys His Cys Ile Gly Thr Trp Ile Val Ser Ala Phe Val
 130 135 140
 Ala Ser Pro Tyr Tyr Ala Tyr Arg Asn Ser His Asp Glu His Glu Cys
 145 150 155 160
 Ile Leu Gly Asn Tyr Thr Trp His Ile Asn Glu Pro Leu His Thr Cys
 165 170 175
 Met Asp Val Val Ile Ile Val Trp Thr Phe Leu Ala Pro Val Leu Val
 180 185 190
 Thr Ile Ile Ala Ser Val Lys Met Arg Arg Thr Thr Trp Gly Asn Thr
 195 200 205
 Arg Leu Asn Glu Lys Asn Ser Asp Ile Leu Ile Val Leu Val Val Met
 210 215 220
 Thr Val Phe Phe Trp Gly Pro Phe Asn Ile Val Leu Val Ile Asp Asn
 225 230 235 240
 Ile Leu Gln Arg Tyr Tyr Asp Thr Thr Asn Cys Asp Val Glu Lys Ile
 245 250 255
 Lys His Ile Met Ala Met Ile Ser Glu Ala Ile Val Tyr Phe Arg Gly
 260 265 270
 Ile Thr Ala Pro Ile Ile Tyr Val Gly Ile Ser Gly Arg Phe Arg Glu
 275 280 285
 Glu Ile Tyr Ser Leu Phe Arg Arg Gln Pro Tyr Asn Asp Leu Asp Pro
 290 295 300
 Asp Ala Asn Gln Phe Met Ile Glu Leu Thr Ser Gln Gly Arg Ser Arg
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 Asn Arg Asn Ala Arg Gln Ser Glu Ser Asn Val Pro Gln Pro Glu Glu
 325 330 335

Cys Phe Trp

<210> 7

<211> 1002

<212> DNA

<213> Rhesus cytomegalovirus

<220>
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 rhUS28.2

<220>
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 <222> (1)..(1002)
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gaaacactag atgcagaaca cgctaaactc atgggttaatt taaaaaacag aaatgctaatt 960
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<210> 8
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 <212> PRT
 <213> Rhesus cytomegalovirus

<220>
 <223> rhesus monkey cytomegalovirus (rhCMV) US28 homolog
 rhUS28.2

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Cys Gly Val Thr Gly Asn Leu Leu Ile Leu Leu Val Leu Phe Thr Arg
      35                      40                      45

Arg Ile His Trp Phe Ala Asn Asp Ile Tyr Tyr Leu Asn Met Ile Phe
      50                      55                      60

Thr Asp Phe Leu Val Phe Ile Thr Leu Pro Ala Trp Val Tyr Tyr Leu
      65                      70                      75                      80

Leu Asn Tyr Thr Gln Leu Ser His Tyr Ala Cys Ile Ala Leu Ser Phe
      85                      90                      95

Val Phe Tyr Val Ser Ile Phe Ile Gln Ala Asp Phe Met Val Ala Val
      100                      105                      110
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 Lys Lys Ala Ser Val Ser Cys Ala Cys Ile Trp Ile Ile Val Ile Ile
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 Val Ser Ser Pro Tyr Tyr Met Phe Arg Ser Gln His Glu Thr Asn Ser
 145 150 155 160
 Cys Ile Leu Gly Asn Tyr Thr Trp His Met Asn Ser Pro Phe Arg Thr
 165 170 175
 Thr Met Asp Ala Ser Ile Asn Ile Trp Ser Phe Val Val Pro Ala Val
 180 185 190
 Thr Thr Leu Leu Ile Ala Arg Arg Ile Tyr Val Cys Thr Ser Gly Asn
 195 200 205
 Lys Lys Met Asn Ala Arg Ala Ser Gly Leu Leu Glu Ala Met Val Ile
 210 215 220
 Ser Met Leu Phe Phe Gly Gly Leu Phe Asn Leu Asn Ile Phe Arg Asp
 225 230 235 240
 Ile Val Ser Asp Thr Ser Glu Asp Asn Lys Asp Cys Thr Tyr Leu Lys
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 Gln Glu His Phe Ile Arg Met Val Gly Val Ala Leu Val Tyr Gly Arg
 260 265 270
 Ala Ile Phe Asn Pro Phe Met Tyr Met Cys Val Ser Thr Arg Leu Arg
 275 280 285
 Gln Glu Ile Lys Cys Leu Phe Met Arg Ile Pro Tyr Glu Thr Leu Asp
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<210> 9
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 <212> DNA
 <213> Rhesus cytomegalovirus

<220>
 <223> rhesus monkey cytomegalovirus (rhCMV) US28 homolog
 rhUS28.3

<220>
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 <222> (1)..(1014)
 <223> rhUS28.3

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<210> 10

<211> 337

<212> PRT

<213> Rhesus cytomegalovirus

<220>

<223> rhesus monkey cytomegalovirus (rhCMV) US28 homolog
rhUS28.3

<400> 10

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Val Val Ile Gly Leu Leu Gly Asn Ile Val Leu Leu Ser Val Leu Val
    35                      40                      45

Val Lys Arg Lys Leu Lys Phe Pro Asn Asp Ile Tyr Phe Phe Asn Ala
    50                      55                      60

Ser Leu Ala Asp Val Phe Ala Val Cys Met Leu Pro Ala Trp Val Asn
    65                      70                      75                      80

Tyr Ala Leu Asp Ser Thr Gln Leu Ser Lys Phe Ser Cys Ile Thr Phe
                85                      90                      95

Thr Phe Gly Phe Tyr Val Ser Leu Phe Ile Gln Ala Trp Met Leu Ile
    100                      105                      110

Leu Val Thr Leu Glu Arg Tyr Gly Ser Leu Val Trp Ile Ala Pro Ile
    115                      120                      125

Thr Arg Asn Lys Ala Ile Ala Asn Cys Val Leu Phe Trp Leu Val Ser
    130                      135                      140

Ile Phe Leu Ala Ala Pro Tyr Tyr Ser Phe Arg Asn Glu Ser Asn Glu
    145                      150                      155                      160

His Gln Cys Ile Met Arg Asn Tyr Thr Trp Ser Val Gly Glu Thr Trp
                165                      170                      175

His Ile Ala Leu Asp Phe Leu Ile Thr Leu Ile Thr Phe Ile Met Pro
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<210> 12

<211> 328

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<213> Rhesus cytomegalovirus

<220>

<223> rhesus monkey cytomegalovirus (rhCMV) US28 homolog
rhUS28.4

<400> 12

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Gly	Pro	Val	Ile	Thr	Gly	Tyr	Thr	Cys	Val	Phe	Leu	Phe	Gly	Ile	Leu
			20					25					30		
Gly	His	Phe	Tyr	Leu	Tyr	Trp	Lys	Asn	His	Gln	Arg	Arg	His	Arg	Thr
		35					40					45			
Asn	Ser	Phe	Ser	Asp	Val	Leu	Phe	Arg	His	Leu	Met	Ile	Thr	Glu	Glu
	50					55					60				
Val	Phe	Thr	Leu	Thr	Ile	Pro	Val	Trp	Ala	Tyr	His	Leu	Thr	Thr	His
65					70				75						80
Gly	Asn	Leu	Pro	Gly	Ser	Trp	Cys	Arg	Ser	Leu	Thr	Phe	Val	Phe	Tyr
				85					90					95	
Leu	Thr	Val	Phe	Ala	Arg	Ala	Phe	Phe	Tyr	Leu	Leu	Leu	Ile	Trp	Asp
			100					105					110		
Arg	Tyr	Ser	Val	Ile	Ile	Cys	Arg	His	Pro	Leu	Pro	Val	Asn	Leu	Asn
		115					120					125			
Tyr	Ser	Gln	Val	Ile	Gly	Leu	Ser	Val	Trp	Leu	Val	Ala	Val	Leu	Ser
	130					135					140				
Ala	Ser	Pro	Phe	Ser	Ile	Phe	Asn	Gly	Ser	Val	Lys	Gln	Cys	Leu	Gly
145					150					155				160	
Asn	Met	Gly	Ser	Ile	Pro	Ser	Glu	Ser	Ser	Ala	Val	Leu	Asn	Leu	Glu
				165					170					175	
Val	His	Leu	Cys	Ser	Phe	Trp	Leu	Pro	Leu	Ile	Met	Ser	Ala	Asn	Cys
			180					185					190		
Tyr	Tyr	Gln	Ala	Lys	Arg	Arg	Ala	Ser	Pro	Asp	Gln	Leu	His	Glu	Leu
		195					200					205			
Tyr	Arg	Cys	Ser	Leu	Leu	Ile	Thr	Ile	Ile	Thr	Thr	Tyr	Ala	Ile	Val
	210					215					220				
Trp	Phe	Pro	Phe	His	Leu	Ala	Leu	Leu	Ile	Asp	Ala	Leu	Ile	Ser	Ile
225					230					235				240	
Ser	His	Val	Glu	Pro	Ser	Ser	Ala	Leu	His	Trp	Ala	Ser	Ile	Val	Val
				245					250					255	

Thr Cys Lys Ser Phe Thr Phe Val Tyr Ala Gly Ile Ser Pro Leu Val
 260 265 270
 Tyr Phe Thr Cys Cys Pro Thr Val Arg Arg Glu Leu Leu Met Ser Leu
 275 280 285
 Arg Pro Phe Phe Thr Trp Ile Ser Ser Lys Thr Arg Arg Gly Tyr Ala
 290 295 300
 Pro Ile Lys Thr Gln Pro Leu Asn Ile Pro Asp Glu Pro Ile Asp Asn
 305 310 315 320
 Lys Ser Pro His Leu Leu Asn Glu
 325

<210> 13
 <211> 1452
 <212> DNA
 <213> Rhesus cytomegalovirus

<220>
 <223> rhesus monkey cytomegalovirus (rhCMV) US28 homolog
 rhUS28.5

<220>
 <221> CDS
 <222> (1)..(1452)
 <223> rhUS28.5

<400> 13
 atgactacca ccacaatgag tgctaccacg aattccagta ccacgcctca agcaagcagc 60
 accacgatga caacgaagac aagcactcct ggcaatacaa ctactggcac tacgtccacc 120
 ctgacaacga tatcaacaac ttctaagtct accagcataa cgtctaattt aagcactacc 180
 ggaaaccaa ctgcaactac caatgctact accttcagtt ccacattaac aacatctaca 240
 aatataagca gtacattttc gacagtttct accgtcgcat ccaatgcaac atgtaattct 300
 acaatcacia cgaatattac aactgctttt actacagcag caaacactac cgcaagcagc 360
 ctcaccagca tcgtaacttc acttgccact accattgaaa ccacatcatt tgattatgat 420
 .gagtcagcag aagcttgcaa cttaacagac atcggtcata ctactagatc agtgacagtt 480
 actttctata ctatcatatt catactcggc cttttgggaa actttctggt tcttatgacc 540
 atcatttgga accgtcgcat ttcttttatg gttgaaatat atttcgttaa tctagcaatc 600
 tccgatctta tgtttgatg tactttacca ttttgataa tgtatcttct tgagcacgac 660
 gtcattgtcac atgcattctg ttagcaatg acagccattt tttattgcgc gctgtttgcc 720
 agcactgttt tctcttgct aattgtttta gacagatggt acgctattct attaggtaca 780
 gaaaaagcaa atagacgttt attgcgcaat gctgtttctg gatgcatgct catgtgggga 840
 ttgtgtttca ttttagcatt acctcatttt atctttatga agaaaggaac caacgtatgt 900
 gtagcagagt atgaaccagg acttaacaat ttctatgtta tttttatcaa tactgaggtg 960
 aacctatgca ccctagtttt gccagccgca gccattatct actggtatct taaactaacc 1020
 aaagcactca aaacccatga acgactgcgt cataggctaa cgtctctaaa catagtgtta 1080
 gctgttgtca ttgtatttgc tttgttttgg ctgccgtata atctcatgct tatgatgtat 1140
 agcttagttc acatgcagat accttgggaa tgcagctctg aaaaaatact gagacgaagt 1200
 ttaattatta cagaatccat cgccctcagt cactgttgca tcaaccccat tatctacttg 1260
 ctcttcggac ctgcgtgtcg aagcgagttc tgtcacctgt tgcgatgttg ctttacgcgc 1320
 ttatgtccac acagatcctg gagttccata cgtgcagaga cgggtgtccat cagtctcagt 1380
 cactcacagg tatctgcatc atctgaggat gatgacaacg atgtgcatga tgaattgcaa 1440
 tttttaattt ga 1452

<210> 14
 <211> 483
 <212> PRT
 <213> Rhesus cytomegalovirus

<220>
 <223> rhesus monkey cytomegalovirus (rhCMV) US28 homolog
 rhUS28.5

<400> 14
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 Gln Ala Ser Ser Thr Thr Met Thr Thr Lys Thr Ser Thr Pro Gly Asn
 20 25 30
 Thr Thr Thr Gly Thr Thr Ser Thr Leu Thr Thr Ile Ser Thr Thr Ser
 35 40 45
 Asn Ala Thr Ser Ile Thr Ser Asn Leu Ser Thr Thr Gly Asn Gln Thr
 50 55 60
 Ala Thr Thr Asn Ala Thr Thr Phe Ser Ser Thr Leu Thr Thr Ser Thr
 65 70 75 80
 Asn Ile Ser Ser Thr Phe Ser Thr Val Ser Thr Val Ala Ser Asn Ala
 85 90 95
 Thr Cys Asn Ser Thr Ile Thr Thr Asn Ile Thr Thr Ala Phe Thr Thr
 100 105 110
 Ala Ala Asn Thr Thr Ala Ser Ser Leu Thr Ser Ile Val Thr Ser Leu
 115 120 125
 Ala Thr Thr Ile Glu Thr Thr Ser Phe Asp Tyr Asp Glu Ser Ala Glu
 130 135 140
 Ala Cys Asn Leu Thr Asp Ile Val His Thr Thr Arg Ser Val Thr Val
 145 150 155 160
 Thr Phe Tyr Thr Ile Ile Phe Ile Leu Gly Leu Leu Gly Asn Phe Leu
 165 170 175
 Val Leu Met Thr Ile Ile Trp Asn Arg Arg Ile Ser Phe Met Val Glu
 180 185 190
 Ile Tyr Phe Val Asn Leu Ala Ile Ser Asp Leu Met Phe Val Cys Thr
 195 200 205
 Leu Pro Phe Trp Ile Met Tyr Leu Leu Glu His Asp Val Met Ser His
 210 215 220
 Ala Ser Cys Val Ala Met Thr Ala Ile Phe Tyr Cys Ala Leu Phe Ala
 225 230 235 240
 Ser Thr Val Phe Leu Leu Leu Ile Val Leu Asp Arg Cys Tyr Ala Ile
 245 250 255
 Leu Leu Gly Thr Glu Lys Ala Asn Arg Arg Leu Leu Arg Asn Ala Val
 260 265 270

Ser Gly Cys Met Leu Met Trp Gly Leu Cys Phe Ile Leu Ala Leu Pro
 275 280 285
 His Phe Ile Phe Met Lys Lys Gly Thr Asn Val Cys Val Ala Glu Tyr
 290 295 300
 Glu Pro Gly Leu Asn Asn Phe Tyr Val Ile Phe Ile Asn Thr Glu Val
 305 310 315 320
 Asn Leu Cys Thr Leu Val Leu Pro Ala Ala Ala Ile Ile Tyr Trp Tyr
 325 330 335
 Leu Lys Leu Thr Lys Ala Leu Lys Thr His Glu Arg Leu Arg His Arg
 340 345 350
 Leu Thr Ser Leu Asn Ile Val Leu Ala Val Val Ile Val Phe Ala Leu
 355 360 365
 Phe Trp Leu Pro Tyr Asn Leu Met Leu Met Met Tyr Ser Leu Val His
 370 375 380
 Met Gln Ile Pro Trp Glu Cys Ser Ser Glu Lys Ile Leu Arg Arg Ser
 385 390 395 400
 Leu Ile Ile Thr Glu Ser Ile Ala Leu Ser His Cys Cys Ile Asn Pro
 405 410 415
 Ile Ile Tyr Leu Leu Phe Gly Pro Arg Cys Arg Ser Glu Phe Cys His
 420 425 430
 Leu Leu Arg Cys Cys Phe Thr Arg Leu Cys Pro His Arg Ser Trp Ser
 435 440 445
 Ser Ile Arg Ala Glu Thr Val Ser Ile Ser Leu Ser His Ser Gln Val
 450 455 460
 Ser Ala Ser Ser Glu Asp Asp Asp Asn Asp Val His Asp Glu Leu Gln
 465 470 475 480
 Phe Leu Ile

<210> 15
 <211> 1296
 <212> DNA
 <213> Human cytomegalovirus

<220>
 <223> human cytomegalovirus (HCMV) AD169 strain open
 reading frame UL78

<220>
 <221> CDS
 <222> (1)..(1296)
 <223> HCMV AD169 UL78

<400> 15
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 gatctactca tcggcatggt cggtccggt agcctgggtca acctgctgac tatcatcggt 180
 tgcctctggg tgttgcggtg tacgcggccg cccgtgtccg tgatgatttt tacttgggaat 240

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ctggtactta gtcagttttt ttccatcctg gccaccatgt tgtccaaggg tatcatgctg 300
cgtggcgctc taaatctcag cctctgtcgc ttagtgctct ttgtcgacga cgtgggccta 360
tattcgacgg cgttggtttt cctcttttctg atactggatc gtctgtcggc catatcttac 420
ggcgtgacg tctggcatca tgagacgcgc gaaaacgcgc gcgtggcgct ctacgcggtc 480
gcctttgcct gggttctttc catcgtagcc gctgtgccc cgcgcgtac gggttcactg 540
gactaccgtt ggctaggctg tcagatccct atacagtatg ccgcggtgga cctcaccatc 600
aagatgtggt ttttgcgtgg ggcgcccatg atcgccgtac tggctaacgt ggtagagttg 660
gcctacagcg atcggcgcga ccacgtctgg tcctacgtgg gtcgtgtctg caccttctac 720
gtgacgtgtc tcatgctggt tgtgccctac tactgcttca gagtcctacg cgggtgtactg 780
cagcccgcga gcgcggccgg caccggtttc ggcatatagg attacgtgga attggctacg 840
cgtacccttc tcaccatgcg tcttggcatt ctgccgtctt ttatcattgc gttcttctcc 900
cgcgagccca ccaaggatct ggatgactcc tttgattatc tggtcgagag atgtcagcaa 960
agctgccacg gtcatttctg acgtcggttg gtgcaggcgt tgaagcgggc tatgtatagc 1020
gtggagctgg ccgtgtgtta cttttctacg tccgtccgag acgtcgccga ggcggtgaaa 1080
aagtcctcca gccgttggtta cgccgacgcg acgtcggcgg ccgttgtggt aacgacaacc 1140
acgtcggaga aagccacgtt ggtggagcac gcggaaggca tggcttccga aatgtgtcct 1200
gggactacga tcgatgtttc ggccgaaagt tcctccgtcc tctgcaccga cggcgaaaac 1260
accgtcgcgt cggacgcgac ggtgacggca ttatga 1296

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<210> 16

<211> 431

<212> PRT

<213> Human cytomegalovirus

<220>

<223> human cytomegalovirus (HCMV) AD169 strain open
reading frame UL78

<400> 16

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Met Ser Pro Ser Val Glu Glu Thr Thr Ser Val Thr Glu Ser Ile Met
 1                      5                      10                      15

Phe Ala Ile Val Ser Phe Lys His Met Gly Pro Phe Glu Gly Tyr Ser
      20                      25                      30

Met Ser Ala Asp Arg Ala Ala Ser Asp Leu Leu Ile Gly Met Phe Gly
      35                      40                      45

Ser Val Ser Leu Val Asn Leu Leu Thr Ile Ile Gly Cys Leu Trp Val
      50                      55                      60

Leu Arg Val Thr Arg Pro Pro Val Ser Val Met Ile Phe Thr Trp Asn
      65                      70                      75                      80

Leu Val Leu Ser Gln Phe Phe Ser Ile Leu Ala Thr Met Leu Ser Lys
      85                      90                      95

Gly Ile Met Leu Arg Gly Ala Leu Asn Leu Ser Leu Cys Arg Leu Val
      100                      105                      110

Leu Phe Val Asp Asp Val Gly Leu Tyr Ser Thr Ala Leu Phe Phe Leu
      115                      120                      125

Phe Leu Ile Leu Asp Arg Leu Ser Ala Ile Ser Tyr Gly Arg Asp Leu
      130                      135                      140

Trp His His Glu Thr Arg Glu Asn Ala Gly Val Ala Leu Tyr Ala Val
      145                      150                      155                      160

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Ala	Phe	Ala	Trp	Val	Leu	Ser	Ile	Val	Ala	Ala	Val	Pro	Thr	Ala	Ala	
				165					170					175		
Thr	Gly	Ser	Leu	Asp	Tyr	Arg	Trp	Leu	Gly	Cys	Gln	Ile	Pro	Ile	Gln	
			180					185					190			
Tyr	Ala	Ala	Val	Asp	Leu	Thr	Ile	Lys	Met	Trp	Phe	Leu	Leu	Gly	Ala	
		195					200					205				
Pro	Met	Ile	Ala	Val	Leu	Ala	Asn	Val	Val	Glu	Leu	Ala	Tyr	Ser	Asp	
	210					215					220					
Arg	Arg	Asp	His	Val	Trp	Ser	Tyr	Val	Gly	Arg	Val	Cys	Thr	Phe	Tyr	
225					230					235					240	
Val	Thr	Cys	Leu	Met	Leu	Phe	Val	Pro	Tyr	Tyr	Cys	Phe	Arg	Val	Leu	
			245						250					255		
Arg	Gly	Val	Leu	Gln	Pro	Ala	Ser	Ala	Ala	Gly	Thr	Gly	Phe	Gly	Ile	
		260						265					270			
Met	Asp	Tyr	Val	Glu	Leu	Ala	Thr	Arg	Thr	Leu	Leu	Thr	Met	Arg	Leu	
	275						280					285				
Gly	Ile	Leu	Pro	Leu	Phe	Ile	Ile	Ala	Phe	Phe	Ser	Arg	Glu	Pro	Thr	
	290					295					300					
Lys	Asp	Leu	Asp	Asp	Ser	Phe	Asp	Tyr	Leu	Val	Glu	Arg	Cys	Gln	Gln	
305					310					315				320		
Ser	Cys	His	Gly	His	Phe	Val	Arg	Arg	Leu	Val	Gln	Ala	Leu	Lys	Arg	
			325						330					335		
Ala	Met	Tyr	Ser	Val	Glu	Leu	Ala	Val	Cys	Tyr	Phe	Ser	Thr	Ser	Val	
			340					345					350			
Arg	Asp	Val	Ala	Glu	Ala	Val	Lys	Lys	Ser	Ser	Ser	Arg	Cys	Tyr	Ala	
		355					360					365				
Asp	Ala	Thr	Ser	Ala	Ala	Val	Val	Val	Thr	Thr	Thr	Thr	Ser	Glu	Lys	
	370					375					380					
Ala	Thr	Leu	Val	Glu	His	Ala	Glu	Gly	Met	Ala	Ser	Glu	Met	Cys	Pro	
385					390					395					400	
Gly	Thr	Thr	Ile	Asp	Val	Ser	Ala	Glu	Ser	Ser	Ser	Val	Leu	Cys	Thr	
			405						410				415			
Asp	Gly	Glu	Asn	Thr	Val	Ala	Ser	Asp	Ala	Thr	Val	Thr	Ala	Leu		
			420					425					430			

<210> 17

<211> 1140

<212> DNA

<213> Rhesus cytomegalovirus

<220>

<223> rhesus monkey cytomegalovirus (rhCMV) UL78 homolog
(rhUL78)

<220>
 <221> CDS
 <222> (1)..(1140)
 <223> rhUL78

<400> 17
 atgattacgg agcgcgtcct cgcaggcatc ctcgcgggca tgacggccgc ggggagtttg 60
 gtcattctcc tcgcggttgt tatgtggttg aacatgttag atcgcgctgg catgccaatg 120
 gccgttgggc attacacagg gaacctggtg ttgactcagg tcatctgtat cttctccatg 180
 ctggcgctca aaattgttgg catgacgagt gcggccaaca tgggcttctg cggcatcgtg 240
 gtttttcttg aagacactgg cctctatgtc acctcgctgc tcttcatgtt tatgatcctg 300
 gatcgcatgg cggttttct taacgggcgt cttttctgga ggcagcagac gacgaagcag 360
 aatctgagta caagcgtgta cattattctg ttttgctggg tgttgggaat ggccgcggct 420
 gttcccagcg cggctgtggc tgcacccaat tccagggtgg aacgctgcga aattccagtg 480
 tcatatgccg caatcgacat gattgtgaag ctctggtttg tgctgttggc acccgctcgtg 540
 ctgattatgg ctgtgatcat tcaatcttcc tatcatcgtg atcgggagag gatctggtac 600
 tatgccagac gtgtgttcat gttctacacg gcctgctttg tcatgatggg gccttattac 660
 ttcgtcagag tcatgctgag cgactttgct ttggttgata taaaaacaaa aacggcgaac 720
 agcgacgggt gtgattcgac atttcttgat tatctgaaca tgttcaactca cgtgatttac 780
 agttttaagt tgggtggtgt tgctttgttc attgtcctgt tttgctccat aaaccgcatg 840
 gaaacgctgg aagaatgctt ggagagggcc gatgctgaga ggcaaagtcg gtcagaagca 900
 tcccagggtg aaaggaggct gccaatcaac acatgctgta taaagttgat tgaattgata 960
 aagcagtatg taagcactct ctctaaagcc acgagggaca attctggcga aagggccaat 1020
 ttgccagaga atgctgaaga tattggaaca actggcagtg atcagctacc gactgaggtc 1080
 accgtgaccc caaattcatc ggctgtgttt agcactggag gaacggtgtc tccagtctaa 1140

<210> 18
 <211> 379
 <212> PRT
 <213> Rhesus cytomegalovirus

<220>
 <223> rhesus monkey cytomegalovirus (rhCMV) UL78 homolog
 (rhUL78)

<400> 18
 Met Ile Thr Glu Arg Val Leu Ala Gly Ile Leu Ala Gly Met Thr Ala
 1 5 10 15
 Ala Gly Ser Leu Val Ile Leu Leu Ala Val Val Met Trp Leu Asn Met
 20 25 30
 Leu Asp Arg Ala Gly Met Pro Met Ala Val Gly His Tyr Thr Gly Asn
 35 40 45
 Leu Val Leu Thr Gln Val Ile Cys Ile Phe Ser Met Leu Ala Ser Lys
 50 55 60
 Ile Val Gly Met Thr Ser Ala Ala Asn Met Gly Phe Cys Gly Ile Val
 65 70 75 80
 Val Phe Leu Glu Asp Thr Gly Leu Tyr Val Thr Ser Leu Leu Phe Met
 85 90 95
 Phe Met Ile Leu Asp Arg Met Ala Ala Phe Leu Asn Gly Arg Leu Phe
 100 105 110
 Trp Arg Gln Gln Thr Thr Lys Gln Asn Leu Ser Thr Ser Val Tyr Ile
 115 120 125

Ile	Leu	Phe	Cys	Trp	Val	Leu	Gly	Met	Ala	Ala	Ala	Val	Pro	Ser	Ala	130	135	140
Ala	Val	Ala	Ala	Pro	Asn	Ser	Arg	Trp	Glu	Arg	Cys	Glu	Ile	Pro	Val	145	150	155
Ser	Tyr	Ala	Ala	Ile	Asp	Met	Ile	Val	Lys	Leu	Trp	Phe	Val	Leu	Leu	165	170	175
Ala	Pro	Val	Val	Leu	Ile	Met	Ala	Val	Ile	Ile	Gln	Ser	Ser	Tyr	His	180	185	190
Arg	Asp	Arg	Glu	Arg	Ile	Trp	Tyr	Tyr	Ala	Arg	Arg	Val	Phe	Met	Phe	195	200	205
Tyr	Thr	Ala	Cys	Phe	Val	Met	Met	Val	Pro	Tyr	Tyr	Phe	Val	Arg	Val	210	215	220
Met	Leu	Ser	Asp	Phe	Ala	Leu	Val	Asp	Ile	Lys	Thr	Lys	Thr	Ala	Asn	225	230	235
Ser	Asp	Gly	Cys	Asp	Ser	Thr	Phe	Leu	Asp	Tyr	Leu	Asn	Met	Phe	Thr	245	250	255
His	Val	Ile	Tyr	Ser	Phe	Lys	Leu	Val	Val	Phe	Ala	Leu	Phe	Ile	Val	260	265	270
Leu	Phe	Cys	Ser	Ile	Asn	Pro	Met	Glu	Thr	Leu	Glu	Glu	Cys	Leu	Glu	275	280	285
Arg	Ala	Asp	Ala	Glu	Arg	Gln	Ser	Arg	Ser	Glu	Ala	Ser	Gln	Gly	Glu	290	295	300
Arg	Arg	Leu	Pro	Ile	Asn	Thr	Cys	Cys	Ile	Lys	Leu	Ile	Glu	Leu	Ile	305	310	315
Lys	Gln	Tyr	Val	Ser	Thr	Leu	Ser	Lys	Ala	Thr	Arg	Asp	Asn	Ser	Gly	325	330	335
Glu	Arg	Ala	Asn	Leu	Pro	Glu	Asn	Ala	Glu	Asp	Ile	Gly	Thr	Thr	Gly	340	345	350
Ser	Asp	Gln	Leu	Pro	Thr	Glu	Val	Thr	Val	Thr	Pro	Asn	Ser	Ser	Ala	355	360	365
Val	Phe	Ser	Thr	Gly	Gly	Thr	Val	Ser	Pro	Val						370	375	

<210> 19

<211> 1173

<212> DNA

<213> Human cytomegalovirus

<220>

<223> human cytomegalovirus (HCMV) AD169 strain open
reading frame UL33

<220>
 <221> CDS
 <222> (1)..(1173)
 <223> HCMV AD169 UL33

<400> 19
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 cttggctatt cgacgcccac catttacatg accaacctct actctactaa ttttctcacg 180
 cttactgtgc taccctttat cgtactcagc aaccagtggc tgttgccggc cggcgtggcc 240
 tcgtgtaaat ttctatcggt gatctactac tcaagctgca cagtgggctt tgccaccgta 300
 gctctgatcg ccgccgatcg ttatcgcgtc cttcataaac gaacatacgc acgccaatca 360
 taccgttcaa cctatatgat tttgctattg acatggctcg ctggactaat tttttccgtg 420
 cccgcagctg tttacaccac ggtggtgatg catcacgatg ccaacgatac caataatact 480
 aatgggcacg ccacctgtgt actgtacttc gtagctgaag aagtgcacac agtgctgctt 540
 tcgtggaaag tgctgctgac gatggtatgg ggtgccgcac ccgtgataat gatgacgtgg 600
 ttctacgcat tcttctactc aaccgtacag cgcacgtcac agaaacaaag gagtcgtacc 660
 ttaacctttg ttagcgtgct actcatctcc ttcgtggcgc taaaaactcc ctacgtctct 720
 ctcgatgatc tcaacagtta tgccacaacc gcctggccca tgcagtgtga acacctcaca 780
 ctgcgacgca ccattggcac gctggcgcgt gtggtgcccc acctacactg cctcattaat 840
 cccatcctgt acgcgctgct gggtcatgat tttctgcaac gcatgcggca gtgtttccgc 900
 ggtcagttgc tggaccgccc cgctttcctg agatcgagc agaatcagcg agctacagcg 960
 gagacaaatc tagcggctgg caacaattca caatcagtgg ctacgtcatt agacaccaat 1020
 agcaaaaact acaatcagca cgccaaacgc agcgtgtctt tcaattttcc cagcgggtacg 1080
 tggaaaggcg gccagaaaac cgcgtccaac gacacatcca caaaaatccc ccatcgactc 1140
 tcacaatcgc atcataacct cagcggggta tga 1173

<210> 20
 <211> 390
 <212> PRT
 <213> Human cytomegalovirus

<220>
 <223> human cytomegalovirus (HCMV) AD169 strain open
 reading frame UL33

<400> 20
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 Thr Phe Ile Ile Phe Val Gly Gly Pro Leu Asn Ala Ile Val Leu Ile
 20 25 30
 Thr Gln Leu Leu Thr Asn Arg Val Leu Gly Tyr Ser Thr Pro Thr Ile
 35 40 45
 Tyr Met Thr Asn Leu Tyr Ser Thr Asn Phe Leu Thr Leu Thr Val Leu
 50 55 60
 Pro Phe Ile Val Leu Ser Asn Gln Trp Leu Leu Pro Ala Gly Val Ala
 65 70 75 80
 Ser Cys Lys Phe Leu Ser Val Ile Tyr Tyr Ser Ser Cys Thr Val Gly
 85 90 95
 Phe Ala Thr Val Ala Leu Ile Ala Ala Asp Arg Tyr Arg Val Leu His
 100 105 110
 Lys Arg Thr Tyr Ala Arg Gln Ser Tyr Arg Ser Thr Tyr Met Ile Leu
 115 120 125

Leu Leu Thr Trp Leu Ala Gly Leu Ile Phe Ser Val Pro Ala Ala Val
 130 135 140
 Tyr Thr Thr Val Val Met His His Asp Ala Asn Asp Thr Asn Asn Thr
 145 150 155 160
 Asn Gly His Ala Thr Cys Val Leu Tyr Phe Val Ala Glu Glu Val His
 165 170 175
 Thr Val Leu Leu Ser Trp Lys Val Leu Leu Thr Met Val Trp Gly Ala
 180 185 190
 Ala Pro Val Ile Met Met Thr Trp Phe Tyr Ala Phe Phe Tyr Ser Thr
 195 200 205
 Val Gln Arg Thr Ser Gln Lys Gln Arg Ser Arg Thr Leu Thr Phe Val
 210 215 220
 Ser Val Leu Leu Ile Ser Phe Val Ala Leu Gln Thr Pro Tyr Val Ser
 225 230 235 240
 Leu Met Ile Phe Asn Ser Tyr Ala Thr Thr Ala Trp Pro Met Gln Cys
 245 250 255
 Glu His Leu Thr Leu Arg Arg Thr Ile Gly Thr Leu Ala Arg Val Val
 260 265 270
 Pro His Leu His Cys Leu Ile Asn Pro Ile Leu Tyr Ala Leu Leu Gly
 275 280 285
 His Asp Phe Leu Gln Arg Met Arg Gln Cys Phe Arg Gly Gln Leu Leu
 290 295 300
 Asp Arg Arg Ala Phe Leu Arg Ser Gln Gln Asn Gln Arg Ala Thr Ala
 305 310 315 320
 Glu Thr Asn Leu Ala Ala Gly Asn Asn Ser Gln Ser Val Ala Thr Ser
 325 330 335
 Leu Asp Thr Asn Ser Lys Asn Tyr Asn Gln His Ala Lys Arg Ser Val
 340 345 350
 Ser Phe Asn Phe Pro Ser Gly Thr Trp Lys Gly Gly Gln Lys Thr Ala
 355 360 365
 Ser Asn Asp Thr Ser Thr Lys Ile Pro His Arg Leu Ser Gln Ser His
 370 375 380
 His Asn Leu Ser Gly Val
 385 390

<210> 21
 <211> 1239
 <212> DNA
 <213> Human cytomegalovirus

<220>
 <223> human cytomegalovirus (HCMV) AD169 strain open
 reading frame UL33 splice variant (UL33 spliced)

<220>
 <221> CDS
 <222> (1)..(1239)
 <223> HCMV AD169 UL33 spliced

<400> 21
 atggacacca tcattccacaa ctcgaccgcg aacaacactc ctccgcacat caatgacact 60
 tgcaacatga cagggccgct attcgccatt cgaaccaccg aagccgtact caacacattc 120
 atcatcttcg tggggcggtcc acttaacgcc atagtgttga tcacgcagct gctcacgaat 180
 cgcgtgcttg gctattcgac gccaccatt tacatgacca acctctactc tactaatttt 240
 ctcacgctta ctgtgctacc ctttatcgta ctcagcaacc agtggctgtt gccggccggc 300
 gtggcctcgt gtaaattttct atcgggtgat tactactcaa gctgcacagt gggctttgcc 360
 accgtagctc tgatcgccgc cgatcgttat cgcgtccttc ataaacgaac atacgcacgc 420
 caatcatacc gttcaacctt tatgattttg ctattgacat ggctcgctgg actaattttt 480
 tccgtgcccg cagctgttta caccacgggt gtgatgcac acgatgccaa cgataccaat 540
 aataactaat ggcacgccac ctgtgtactg tacttcgtag ctgaagaagt gcacacagt 600
 ctgctttcgt ggaaagtgtc gctgacgatg gtatgggggt cgcaccccg gataatgatg 660
 acgtgggtct acgcattctt ctactcaacc gtacagcgca cgtcacagaa acaaaggagt 720
 cgtaccttaa cctttggttag cgtgctactc atctccttcg tggcgctaca aactccctac 780
 gtctctctca tgatcttcaa cagttatgcc acaaccgcct ggcccatgca gtgtgaacac 840
 ctcacactgc gacgcaccat tggcacgctg gcgcgtgtgg tgccccacct acactgcctc 900
 attaatccca tcctgtacgc gctgctgggt catgattttc tgcaacgcat gcggcagtgt 960
 ttccgcggtc agttgctgga ccgcgcgctt ttctgagat cgcagcagaa tcagcgagct 1020
 acagcggaga caaatctagc ggctggcaac aattcacaat cagtggctac gtcattagac 1080
 accaatagca aaaactacaa tcagcacgcc aaacgcagcg tgtctttcaa ttttcccagc 1140
 ggtacgtgga aaggcggcca gaaaaccgcg tccaacgaca catccacaaa aatcccccat 1200
 cgactctcac aatcgcatca taacctcagc ggggtatga 1239

<210> 22
 <211> 412
 <212> PRT
 <213> Human cytomegalovirus

<220>
 <223> human cytomegalovirus (HCMV) AD169 strain open
 reading frame UL33 splice variant (UL33 spliced)

<400> 22
 Met Asp Thr Ile Ile His Asn Ser Thr Arg Asn Asn Thr Pro Pro His
 1 5 10 15
 Ile Asn Asp Thr Cys Asn Met Thr Gly Pro Leu Phe Ala Ile Arg Thr
 20 25 30
 Thr Glu Ala Val Leu Asn Thr Phe Ile Ile Phe Val Gly Gly Pro Leu
 35 40 45
 Asn Ala Ile Val Leu Ile Thr Gln Leu Leu Thr Asn Arg Val Leu Gly
 50 55 60
 Tyr Ser Thr Pro Thr Ile Tyr Met Thr Asn Leu Tyr Ser Thr Asn Phe
 65 70 75 80
 Leu Thr Leu Thr Val Leu Pro Phe Ile Val Leu Ser Asn Gln Trp Leu
 85 90 95
 Leu Pro Ala Gly Val Ala Ser Cys Lys Phe Leu Ser Val Ile Tyr Tyr
 100 105 110

Ser Ser Cys Thr Val Gly Phe Ala Thr Val Ala Leu Ile Ala Ala Asp
 115 120 125
 Arg Tyr Arg Val Leu His Lys Arg Thr Tyr Ala Arg Gln Ser Tyr Arg
 130 135 140
 Ser Thr Tyr Met Ile Leu Leu Leu Thr Trp Leu Ala Gly Leu Ile Phe
 145 150 155 160
 Ser Val Pro Ala Ala Val Tyr Thr Thr Val Val Met His His Asp Ala
 165 170 175
 Asn Asp Thr Asn Asn Thr Asn Gly His Ala Thr Cys Val Leu Tyr Phe
 180 185 190
 Val Ala Glu Glu Val His Thr Val Leu Leu Ser Trp Lys Val Leu Leu
 195 200 205
 Thr Met Val Trp Gly Ala Ala Pro Val Ile Met Met Thr Trp Phe Tyr
 210 215 220
 Ala Phe Phe Tyr Ser Thr Val Gln Arg Thr Ser Gln Lys Gln Arg Ser
 225 230 235 240
 Arg Thr Leu Thr Phe Val Ser Val Leu Leu Ile Ser Phe Val Ala Leu
 245 250 255
 Gln Thr Pro Tyr Val Ser Leu Met Ile Phe Asn Ser Tyr Ala Thr Thr
 260 265 270
 Ala Trp Pro Met Gln Cys Glu His Leu Thr Leu Arg Arg Thr Ile Gly
 275 280 285
 Thr Leu Ala Arg Val Val Pro His Leu His Cys Leu Ile Asn Pro Ile
 290 295 300
 Leu Tyr Ala Leu Leu Gly His Asp Phe Leu Gln Arg Met Arg Gln Cys
 305 310 315 320
 Phe Arg Gly Gln Leu Leu Asp Arg Arg Ala Phe Leu Arg Ser Gln Gln
 325 330 335
 Asn Gln Arg Ala Thr Ala Glu Thr Asn Leu Ala Ala Gly Asn Asn Ser
 340 345 350
 Gln Ser Val Ala Thr Ser Leu Asp Thr Asn Ser Lys Asn Tyr Asn Gln
 355 360 365
 His Ala Lys Arg Ser Val Ser Phe Asn Phe Pro Ser Gly Thr Trp Lys
 370 375 380
 Gly Gly Gln Lys Thr Ala Ser Asn Asp Thr Ser Thr Lys Ile Pro His
 385 390 395 400
 Arg Leu Ser Gln Ser His His Asn Leu Ser Gly Val
 405 410

<210> 23
 <211> 990
 <212> DNA
 <213> Rhesus cytomegalovirus

<220>
 <223> rhesus monkey cytomegalovirus (rhCMV) UL33 homolog
 (rhUL33)

<220>
 <221> CDS
 <222> (1) .. (990)
 <223> rhUL33

<400> 23
 atgaccaatc tttactctgc caatthttctc accttgatag tacttccttt tategtttta 60
 agcaatcaac acctthttacc tgccagtgc gtaacctgta aatttctctc cctggtgtac 120
 tactctagct gcagcgtagg ttttgctaca gtggcactga tagcggccga ccgataccga 180
 gtgattcatc gccgaactca agctcgccaa tcctaccgta acacatatat gatagtaggc 240
 ttaacgtggc tcattggctt gatctgcgct acccccgggg ggggtctacac aaccattgta 300
 gctcaccgcg atggggaaag tgatgctcaa agacacaata cttgcattat gcactttgcg 360
 tatgatgaag tttacgtcct catggtctgg aaacttctca tcgttttagt ctgggggcata 420
 gtgccagttg tcatgatgag ctgggttttac gcgttttttt acaataactgt acaaagaaca 480
 gccaaaaaac aacaacgtac gttgaaattc gtaaagggtat tactcctgtc attcatcatc 540
 atccaaactc cctatgtgtc aatcatgatt tttaacacgt atgccaccgt aggatggccg 600
 atggaatgcg ccgatctaac tagacgccga gtcatacaaa cgttttcccg tctcgtcccc 660
 aatctacatt gcattggtcaa ccccatcctc tacgctctca tgggaaatga ctttgtgtct 720
 aaagtggggc aatgcttttcg ggggggaactc acgaaccgtc gaacttttct gcgttccaag 780
 caacaagccc gcaactcgga cgatgtaccg acaattgtca gtcaacaacc cgccacaccc 840
 accatcgtca ataagcccga aaaaaacccg cacgtaaaac gcggtgtatc tttcagcgtc 900
 agcgcattct ccgaactcgc agcggccaaa aaagccaaag acaaagccaa gcggcctttcc 960
 atgtcccacc aaaacctacg tctgacgtga 990

<210> 24
 <211> 329
 <212> PRT
 <213> Rhesus cytomegalovirus

<220>
 <223> rhesus monkey cytomegalovirus (rhCMV) UL33 homolog
 (rhUL33)

<400> 24
 Met Thr Asn Leu Tyr Ser Ala Asn Phe Leu Thr Leu Ile Val Leu Pro
 1 5 10 15
 Phe Ile Val Leu Ser Asn Gln His Leu Leu Pro Ala Ser Ala Val Thr
 20 25 30
 Cys Lys Phe Leu Ser Leu Leu Tyr Tyr Ser Ser Cys Ser Val Gly Phe
 35 40 45
 Ala Thr Val Ala Leu Ile Ala Ala Asp Arg Tyr Arg Val Ile His Arg
 50 55 60
 Arg Thr Gln Ala Arg Gln Ser Tyr Arg Asn Thr Tyr Met Ile Val Gly
 65 70 75 80
 Leu Thr Trp Leu Ile Gly Leu Ile Cys Ala Thr Pro Gly Gly Val Tyr
 85 90 95

Thr Thr Ile Val Ala His Arg Asp Gly Glu Ser Asp Ala Gln Arg His
 100 105 110
 Asn Thr Cys Ile Met His Phe Ala Tyr Asp Glu Val Tyr Val Leu Met
 115 120 125
 Val Trp Lys Leu Leu Ile Val Leu Val Trp Gly Ile Val Pro Val Val
 130 135 140
 Met Met Ser Trp Phe Tyr Ala Phe Phe Tyr Asn Thr Val Gln Arg Thr
 145 150 155 160
 Ala Lys Lys Gln Gln Arg Thr Leu Lys Phe Val Lys Val Leu Leu Leu
 165 170 175
 Ser Phe Ile Ile Ile Gln Thr Pro Tyr Val Ser Ile Met Ile Phe Asn
 180 185 190
 Thr Tyr Ala Thr Val Gly Trp Pro Met Glu Cys Ala Asp Leu Thr Arg
 195 200 205
 Arg Arg Val Ile Asn Thr Phe Ser Arg Leu Val Pro Asn Leu His Cys
 210 215 220
 Met Val Asn Pro Ile Leu Tyr Ala Leu Met Gly Asn Asp Phe Val Ser
 225 230 235 240
 Lys Val Gly Gln Cys Phe Arg Gly Glu Leu Thr Asn Arg Arg Thr Phe
 245 250 255
 Leu Arg Ser Lys Gln Gln Ala Arg Asn Ser Asp Asp Val Pro Thr Ile
 260 265 270
 Val Ser Gln Gln Pro Ala Thr Pro Thr Ile Val Asn Lys Pro Glu Lys
 275 280 285
 Asn Pro His Val Lys Arg Gly Val Ser Phe Ser Val Ser Ala Ser Ser
 290 295 300
 Glu Leu Ala Ala Ala Lys Lys Ala Lys Asp Lys Ala Lys Arg Leu Ser
 305 310 315 320
 Met Ser His Gln Asn Leu Arg Leu Thr
 325

<210> 25
 <211> 1328
 <212> DNA
 <213> Rhesus cytomegalovirus

 <220>
 <223> rhesus monkey cytomegalovirus (rhCMV) UL33 splice
 variant homolog (rhUL33 spliced)

 <220>
 <221> CDS
 <222> (1)..(1328)
 <223> rhUL33 spliced

<400> 25
atggcagtca ctttacgagg cggcagcccg ataaacttta aactcatgat tgtcagccac 60
agaaaccgga aatttcacga gatacggctg tttcagcggt ctgctatccg tccaggcggg 120
ttatggaaac cattcttcac aaccgaacga gtgaaactaa ttccattttg cacatcaaca 180
ccacctgcaa tgtgaccgac tcaactgtac cgcgcaaaact aggcgaagcc ctcgtgaaca 240
gcgcgctagc tttattcggt acccccctca acgccatcgt cctcgtcaca cagctattgg 300
ccaaccgagt tcatggatac tccaccccgga ttatctacat gaccaatctt tactctgcca 360
atcttctcac cttgatagta cttcctttta tcgttttaag caatcaacac cttttacctg 420
ccagtgcagt aacctgtaaa tttctctccc tgttgacta ctctagctgc agcgtagggt 480
ttgctacagt ggcactgata gcggccgacc gataccgagt gattcatcgc cgaactcaag 540
ctcgccaatc ctaccgtaac acatatatga tagtaggctt aacgtggctc attggcctga 600
tctgcgtac ccccgggggg gtctacacaa ccattgtagc tcaccgcat ggggaaagtg 660
atgctcaaag acacaatact tgcattatgc actttgcgta tgatgaagt tacgtcctca 720
tggtctggaa acttctcatc gttttagtct ggggcatagt gccagttgtc atgatgagct 780
ggttttacgc gtttttttac aatactgtac aaagaacagc caaaaaacaa caacgtacgt 840
tgaaattcgt aaaggtatta ctctgtcat tcatcatcat ccaaactccc tatgtgtcaa 900
tcatgatttt taacacgtat gccaccgtag gatggccgat ggaatgcgcc gatctaacta 960
gacgccgagt catcaacacg ttttcccgtc tcgtcccaa tctacattgc atggtcaacc 1020
ccatcctcta cgtctcatg ggaaatgact ttgtgtctaa agtgggccaa tgctttcggg 1080
gggaactcac gaaccgtcga acttttctgc gttccaagca acaagccgc aactcggacg 1140
atgtaccgac aattgtcagt caacaaccg ccacaccac catcgtcaat aagcccgaag 1200
aaaaccgca cgtaaaacgc ggtgtatctt tcagcgtcag cgcattctcc gaactcgcag 1260
cggccaaaaa agccaaagac aaagccaagc ggctttccat gtcccaccaa aacctacgtc 1320
tgacgtga 1328

<210> 26
<211> 441
<212> PRT
<213> Rhesus cytomegalovirus

<220>
<223> rhesus monkey cytomegalovirus (rhCMV) UL33 splice
variant homolog (rhUL33 spliced)

<400> 26
Met Ala Val Thr Leu Arg Gly Gly Ser Pro Ile Asn Phe Lys Leu Met
1 5 10 15
Ile Val Ser His Arg Asn Arg Lys Phe His Glu Ile Arg Leu Phe Gln
20 25 30
Arg Ser Ala Ile Arg Pro Gly Gly Leu Trp Lys Pro Phe Phe Thr Thr
35 40 45
Glu Arg Glu Thr Asn Ser Ile Leu His Ile Asn Thr Thr Cys Asn Val
50 55 60
Thr Asp Ser Leu Tyr Ala Ala Lys Leu Gly Glu Ala Leu Val Asn Ser
65 70 75 80
Ala Leu Ala Leu Phe Gly Thr Pro Leu Asn Ala Ile Val Leu Val Thr
85 90 95
Gln Leu Leu Ala Asn Arg Val His Gly Tyr Ser Thr Pro Ile Ile Tyr
100 105 110
Met Thr Asn Leu Tyr Ser Ala Asn Phe Leu Thr Leu Ile Val Leu Pro
115 120 125

Phe Ile Val Leu Ser Asn Gln His Leu Leu Pro Ala Ser Ala Val Thr
 130 135 140
 Cys Lys Phe Leu Ser Leu Leu Tyr Tyr Ser Ser Cys Ser Val Gly Phe
 145 150 155 160
 Ala Thr Val Ala Leu Ile Ala Ala Asp Arg Tyr Arg Val Ile His Arg
 165 170 175
 Arg Thr Gln Ala Arg Gln Ser Tyr Arg Asn Thr Tyr Met Ile Val Gly
 180 185 190
 Leu Thr Trp Leu Ile Gly Leu Ile Cys Ala Thr Pro Gly Gly Val Tyr
 195 200 205
 Thr Thr Ile Val Ala His Arg Asp Gly Glu Ser Asp Ala Gln Arg His
 210 215 220
 Asn Thr Cys Ile Met His Phe Ala Tyr Asp Glu Val Tyr Val Leu Met
 225 230 235 240
 Val Trp Lys Leu Leu Ile Val Leu Val Trp Gly Ile Val Pro Val Val
 245 250 255
 Met Met Ser Trp Phe Tyr Ala Phe Phe Tyr Asn Thr Val Gln Arg Thr
 260 265 270
 Ala Lys Lys Gln Gln Arg Thr Leu Lys Phe Val Lys Val Leu Leu Leu
 275 280 285
 Ser Phe Ile Ile Ile Gln Thr Pro Tyr Val Ser Ile Met Ile Phe Asn
 290 295 300
 Thr Tyr Ala Thr Val Gly Trp Pro Met Glu Cys Ala Asp Leu Thr Arg
 305 310 315 320
 Arg Arg Val Ile Asn Thr Phe Ser Arg Leu Val Pro Asn Leu His Cys
 325 330 335
 Met Val Asn Pro Ile Leu Tyr Ala Leu Met Gly Asn Asp Phe Val Ser
 340 345 350
 Lys Val Gly Gln Cys Phe Arg Gly Glu Leu Thr Asn Arg Arg Thr Phe
 355 360 365
 Leu Arg Ser Lys Gln Gln Ala Arg Asn Ser Asp Asp Val Pro Thr Ile
 370 375 380
 Val Ser Gln Gln Pro Ala Thr Pro Thr Ile Val Asn Lys Pro Glu Lys
 385 390 395 400
 Asn Pro His Val Lys Arg Gly Val Ser Phe Ser Val Ser Ala Ser Ser
 405 410 415
 Glu Leu Ala Ala Ala Lys Lys Ala Lys Asp Lys Ala Lys Arg Leu Ser
 420 425 430
 Met Ser His Gln Asn Leu Arg Leu Thr
 435 440

<210> 27
 <211> 2100
 <212> DNA
 <213> Rhesus cytomegalovirus

<220>
 <223> rhesus monkey cytomegalovirus (rhCMV) UL33 splice
 variant homolog (rhUL33 spliced) nucleotide
 sequence segment that extends 1000 nucleotides
 upstream and downstream of the rhUL33 reading
 frame

<220>
 <221> exon
 <222> (603)..(752)
 <223> exon 1

<220>
 <221> intron
 <222> (753)..(830)

<220>
 <221> exon
 <222> (831)..(2006)
 <223> exon 2

<220>
 <221> misc_feature
 <222> (1017)..(2006)
 <223> unspliced gene

<400> 27
 cggccaagat gtcccaagag gttctgacat gaacaatcac ttttcgaga tagatgagtt 60
 tgtagtgagg atttaccaga gaactattgg agtgacgctc aagatgaagc ttcactggcc 120
 gtatttcgaa catattgtta gatatagcta gtaaagaatc ttctaaagcc atgacgtctt 180
 tctgacgaag ttgaataaat tctatctcac cagtacccaa aggctgacac tcagacaact 240
 ttgccaaggc cggttgacccc accatggcat tctgaatcac agtaacatcc gtccgagaat 300
 cgtcaccaaa aacggtggcc tccaaagtgc gcagggtgagg ccgagccttt actggatctc 360
 ggaagggata catgtgtgct cgccgagtga cagcattagc attaacctca aactcatcta 420
 aaagcgatga taaatcagga atatgatagc gcaattctcg atagtaggcc aaccagagga 480
 ctaattgggt gaacagacag ctccgtctgt gcaaaaactt ttgcgcgcat tttctgagaa 540
 ttttaggatg ctgctctaaa tctacgttct cttagtcgg cagggtcttt aaaaagttag 600
 tgatggcagt cactttacga ggccgagcc cgataaactt taaactcatg attgtcagcc 660
 acagaaaccg gaaatttcac gagatacggc tgtttcagcg ttctgctatc cgtccaggcg 720
 gggtatggaa accattcttc acaaccgaac ggtgagtgac atttaagaca gtttaatagc 780
 caacactcgt aacgtctcgg aagctgataa gtttcgtttt tccacagagt gaaactaatt 840
 ccattttgca catcaacacc acctgcaatg tgaccgactc actgtacgcc gccaaactag 900
 gcgaagccct cgtgaacagc gcgtagctt tattcggtac cccctcaac gccatcgccc 960
 tcgtcacaca gctattggcc aaccgagttc atggatactc caccocgatt atctacatga 1020
 ccaatcttta ctctgccaat tttctcacct tgatagtact tctttttatc gttttaagca 1080
 atcaacacct tttacctgcc agtgcagtaa cctgtaaatt tctctccctg ttgtactact 1140
 ctagtctcag cgtagggttt gctacagtgg cactgatagc ggccgaccga taccgagtga 1200
 ttcacgcgcg aactcaagct cgccaatcct accgtaacac atatatgata gtaggcttaa 1260
 cgtggctcat tggcttgatc tgcgctaccc ccgggggggt ctacacaacc attgtagctc 1320
 accgcgatgg ggaaagtgat gctcaaagac acaatacttg cattatgcac tttgcgtatg 1380
 atgaagttta cgtcctcatg gtctggaaac ttctcatcgt ttagtcttgg ggcatagtgc 1440
 cagttgtcat gatgagctgg ttttacgcgt ttttttacia tactgtacaa agaacagcca 1500
 aaaaacaaca acgtacgttg aaattcgtaa aggtattact cctgtcattc atcatcatcc 1560
 aaactcccta tgtgtcaatc atgattttta acacgtatgc caccgtagga tggccgatgg 1620
 aatgcgccga tctaactaga cgccgagtca tcaacacgtt ttcccgtctc gtccccaatc 1680
 tacattgcat ggtcaacccc atcctctacg ctctcatggg aaatgacttt gtgtctaaag 1740

tgggccaatg ctttcggggg gaactcacga accgtcgaac ttttctgcgt tccaagcaac 1800
aagcccgcga ctcggacgat gtaccgacaa ttgtcagtca acaaccgcc acaccacca 1860
tcgtcaataa gcccgaaaaa aaccgcacg taaaacgcgg tgtatcttc agcgtcagcg 1920
catcttccga actcgcagcg gccaaaaaag ccaaagacaa agccaagcgg ctttccatgt 1980
cccacaaaaa cctacgtctg acgtgaattt tcctagaggc tgccctccacg ggtttacata 2040
catatctcgg tacttgctac acttgatcac tttactgcgg acaccacggc caatcgcac 2100

<210> 28
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog
rhUS28.1 amplification primer sequence (upper
strand)

<400> 28
tatgaataac acatcttgca acttc 25

<210> 29
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog
rhUS28.1 amplification primer sequence (lower
strand)

<400> 29
cacacagacc acatgtac 18

<210> 30
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog
rhUS28.2 amplification primer sequence (upper
strand)

<400> 30
attcaacatg accaacgccg g 21

<210> 31
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog
rhUS28.2 amplification primer sequence (lower
strand)

<400> 31 gcatttcggt ggattcg	17
<210> 32 <211> 16 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence:rhUS28 homolog rhUS28.3 amplification primer sequence (upper strand)	
<400> 32 catgaccaac actaac	16
<210> 33 <211> 16 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence:rhUS28 homolog rhUS28.3 amplification primer sequence (lower strand)	
<400> 33 gagtcttttg tgagcc	16
<210> 34 <211> 19 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence:rhUS28 homolog rhUS28.4 amplification primer sequence (upper strand)	
<400> 34 tatgaattcg agccagcac	19
<210> 35 <211> 19 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence:rhUS28 homolog rhUS28.4 amplification primer sequence (lower strand)	
<400> 35 gtacgcgact aagacagag	19

<210> 36
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:rhUS28 homolog
 rhUS28.5 amplification primer sequence (upper
 strand)

 <400> 36
 aaagatgact accaccac 18

 <210> 37
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:rhUS28 homolog
 rhUS28.5 amplification primer sequence (lower
 strand)

 <400> 37
 ataacctagc acctcccc 18

 <210> 38
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:rhUS28 homolog
 rhUL78 amplification primer sequence (upper
 strand)

 <400> 38
 ctgaaacat gattacgg 18

 <210> 39
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:rhUS28 homolog
 rhUL78 amplification primer sequence (lower
 strand)

 <400> 39
 cacgcagcac aagagcac 18

 <210> 40
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:rhUS28 homolog
 rhUL33 amplification primer sequence (upper
 strand)

<400> 40
 catgaccaat ctttactc 18

<210> 41
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:rhUS28 homolog
 rhUL33 amplification primer sequence (lower
 strand)

<400> 41
 gtgtcgccac tcctaccc 18

<210> 42
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:rhUS28 homolog
 rhUL33 splice amplification primer sequence (upper
 strand)

<400> 42
 aagttagtga tggcagtc 18

<210> 43
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:rhUS28 homolog
 rhUL33 splice amplification primer sequence (lower
 strand)

<400> 43
 gtatgtaaac ccgtggag 18

<210> 44
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:nested PCR CMV
 specific primer able to amplify the rhCMV
 immediate early 2 gene

<400> 44
gccaatgcat cctctggatg tattgtga

28

<210> 45
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nested PCR CMV
specific primer able to amplify the rhCMV
immediate early 2 gene

<400> 45
tgcttgggga atctctgcac

20

<210> 46
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nested PCR CMV
specific primer able to amplify the rhCMV
immediate early 2 gene

<400> 46
cccttctga ctactaatgt ac

22

<210> 47
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nested PCR CMV
specific primer able to amplify the rhCMV
immediate early 2 gene

<400> 47
ttggggaatc tctgcacaag

20

<210> 48
<211> 354
<212> PRT
<213> Human cytomegalovirus

<220>
<223> human cytomegalovirus (HCMV) AD169 strain open
reading frame US28

<400> 48
Met Thr Pro Thr Thr Thr Thr Ala Glu Leu Thr Thr Glu Phe Asp Tyr
1 5 10 15
Asp Glu Asp Ala Thr Pro Cys Val Phe Thr Asp Val Leu Asn Gln Ser
20 25 30

Lys Pro Val Thr Leu Phe Leu Tyr Gly Val Val Phe Leu Phe Gly Ser
 35 40 45
 Ile Gly Asn Phe Leu Val Ile Phe Thr Ile Thr Trp Arg Arg Arg Ile
 50 55 60
 Gln Cys Ser Gly Asp Val Tyr Phe Ile Asn Leu Ala Ala Ala Asp Leu
 65 70 75 80
 Leu Phe Val Cys Thr Leu Pro Leu Trp Met Gln Tyr Leu Leu Asp His
 85 90 95
 Asn Ser Leu Ala Ser Val Pro Cys Thr Leu Leu Thr Ala Cys Phe Tyr
 100 105 110
 Val Ala Met Phe Ala Ser Leu Cys Phe Ile Thr Glu Ile Ala Leu Asp
 115 120 125
 Arg Tyr Tyr Ala Ile Val Tyr Met Arg Tyr Arg Pro Val Lys Gln Ala
 130 135 140
 Cys Leu Phe Ser Ile Phe Trp Trp Ile Phe Ala Val Ile Ile Ala Ile
 145 150 155 160
 Pro His Phe Met Val Val Thr Lys Lys Asp Asn Gln Cys Met Thr Asp
 165 170 175
 Tyr Asp Tyr Leu Glu Val Ser Tyr Pro Ile Ile Leu Asn Val Glu Leu
 180 185 190
 Met Leu Gly Ala Phe Val Ile Pro Leu Ser Val Ile Ser Tyr Cys Tyr
 195 200 205
 Tyr Arg Ile Ser Arg Ile Val Ala Val Ser Gln Ser Arg His Lys Gly
 210 215 220
 Arg Ile Val Arg Val Leu Ile Ala Val Val Leu Val Phe Ile Ile Phe
 225 230 235 240
 Trp Leu Pro Tyr His Leu Thr Leu Phe Val Asp Thr Leu Lys Leu Leu
 245 250 255
 Lys Trp Ile Ser Ser Ser Cys Glu Phe Glu Arg Ser Leu Lys Arg Ala
 260 265 270
 Leu Ile Leu Thr Glu Ser Leu Ala Phe Cys His Cys Cys Leu Asn Pro
 275 280 285
 Leu Leu Tyr Val Phe Val Gly Thr Lys Phe Arg Gln Glu Leu His Cys
 290 295 300
 Leu Leu Ala Glu Phe Arg Gln Arg Leu Phe Ser Arg Asp Val Ser Trp
 305 310 315 320
 Tyr His Ser Met Ser Phe Ser Arg Arg Ser Ser Pro Ser Arg Arg Glu
 325 330 335
 Thr Ser Ser Asp Thr Leu Ser Asp Glu Val Cys Arg Val Ser Gln Ile
 340 345 350
 Ile Pro